AMENDMENTS TO CLAIMS

1. (Currently amended) A mass analysis method comprising:

~~selecting an~~ obtaining amino acid ~~sequence~~ sequences from protein information ~~and peptide information~~ stored in a database;

estimating [[each]] a mass ~~corresponding to~~ for each of said amino acid ~~sequence information~~ sequences;

calculating a number of ~~amino acid sequences~~ occurrences for each of said [[mass]] masses;

subsequently, obtaining a mass spectrum by performing an MS analysis of a sample with a mass analysis apparatus ~~after the calculating of the number of amino acid sequences~~;

selecting a precursor ion based on the obtained mass spectrum and the [[number]] calculated numbers of ~~amino acid sequences~~ occurrences;

performing an MS/MS analysis of the selected precursor ion; and

performing an identification process using a mass spectrum obtained through the MS/MS analysis.

2. (Original) The mass analysis method according to claim 1, further comprising, when the mass of the component information obtained from said database is estimated, estimating a peptide that will be obtained by enzymatically digesting each protein with a predetermined digestive enzyme, and estimating the mass of each peptide.

3. (Original) The mass analysis method according to claim 1, further comprising pre-setting the number of said precursor ions that are selected.

4. (Currently amended) A mass analysis method whereby a sample is ionized and a protein is analyzed using a mass analysis apparatus, comprising the steps of:

(A) obtaining information about a plurality of proteins from an external database in which information about proteins is stored;

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(B) estimating ~~the mass~~ masses of peptides corresponding to said ~~each of said obtained plurality of~~ proteins;

(C) calculating a weight pattern by conducting normalization such that 1 is given when there is [[said]] an estimated mass and 0 is given when there is no [[such]] estimated mass~~, summing the estimation results for all of the proteins so as to determine a frequency for each mass~~;

(D) measuring a sample and acquiring a mass spectrum;

(E) normalizing the spectrum of the sample such that 1 is given ~~when there is a~~ for each mass, when there is a mass, and 0 is given when there is no mass;

(F) creating a pseudospectrum by superposing said spectrum of an actual sample that has been normalized on said weight pattern; and

(G) selecting a precursor ion to be subjected to MS/MS analysis from said mass spectrum of said sample based on the created pseudospectrum.

5. (Currently amended) The mass analysis method according to claim 4, further comprising creating, when said weight pattern is calculated, a first pattern in which masses of lower frequencies are emphasized ~~for weighting in order of decreasing frequency~~ and a second pattern in which masses of higher frequencies are emphasized ~~for weighting in order of increasing frequency~~.

6. (Original) The mass analysis method according to claim 5, wherein the mass for which the weighting value indicates the highest value in said second pattern is eliminated when the precursor ion to be subjected to MS/MS analysis is selected.

7. (Original) The mass analysis method according to claim 4, wherein a plurality of conditions are set when information is obtained from said database, and said steps (B) and (C) are performed for each item of information obtained in accordance with each of said set conditions, and the difference in frequency of the weight patterns according to each of said set conditions is determined so as to obtain a new weight pattern.

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8. (Currently amended) A mass analysis apparatus comprising:

an ionization unit for ionizing a sample;

a mass analysis unit for performing mass analysis; and

a data processing unit for setting analysis conditions and performing data processing on an analysis result,

wherein the data processing unit performs

a preparation process in which, in accordance with a preset condition, [[an]] amino acid ~~sequence is selected~~ sequences are obtained from protein information ~~and peptide information~~ stored in a database, [[each]] a mass is estimated for ~~corresponding to~~ each of said amino acid ~~sequence information is estimated~~ sequences, and a number of ~~amino acid sequences~~ occurrences is calculated for each mass ~~is calculated~~, and

a precursor ion selection process in which, after the preparation process, a precursor ion to be subjected to MS/MS analysis is selected in light of a mass spectrum obtained through a mass analysis of an actual sample and in accordance with the calculated ~~number~~ numbers of ~~amino acid sequences~~ occurrences.

9. (Previously presented) The mass analysis apparatus according to claim 8, wherein said data processing unit comprises a display unit, wherein said display unit displays said number of amino acid sequences for each of the masses, wherein said mass spectrum obtained by mass analysis of said actual sample is superposed on the displayed contents.

10. (Original) The mass analysis apparatus according to claim 8, wherein whether or not each of the peaks in said mass spectrum obtained by mass analysis of said actual sample has been selected as a precursor ion is displayed.

11. (Previously presented) The mass analysis method according to claim 4, further comprising designating a range of intensity of the pseudospectrum, and selecting the precursor ion within the designated range in order of decreasing intensity.